



FIGURE 1

CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAAATATTTTAAATATT
AATATACATTCTCTCTGTCAGAAATACATAAACTTTATTATATCAGCGCAGG
GCGGCGCGGCGTCGGTCCCGGGAGCAGAACCCGGCTTTTTCTTGGAGCGACG
CTGTCTCTAGTCGCTGATCCCAATGACCGGCTCATCTTTGTCTACACTCTA
ATCTGCGCAAACTTTTGCAGCTGTCTGGGACACTTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
CTACGTGCAGAGTCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTG
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTGACA
ATCAGTTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGT
GGAAGTTGAAGATATATCCGAAACCAAGTACCATTATTAGAGGACGATGGTGT
GGACACAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAACCAAATTTAA
ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATTTA
TTATCTTTGCTGGAAGATTTCACCCCGCAGCAGCTTCAGAGACCAACTGGG
AATCTGTCACAAGCTCTATTTCAAGGGGTATCCTATAACTCTCCATCAGTAACG
GATCCCACTCTGATTGCGGATGCTCTGGACAAAAAATTGCAGAAATTTGATA
CAGTGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT
TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTTCATACCATGAC
CGGAAGTCAAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA
GTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC
CAATGTGGTCTCTTTCCACGTTGCCTCCTCGTGACGCGCTGTGGAGGAAAT
GTGGCTGTGGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAAC
CGTGA AAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGG
AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGA
AACGATGTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
CATCCTTACATTAAGCCTGAAAGAACCCTTAGTTTAAAGGAGGGTGAGATAAG
AGACCCTTTTCTACCAGCAACCAAACCTTACTACTAGCCTGCAATGCAATGA
ACACAAGTGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAG
AAAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAAT
AGTGTGTGAGGTATATATGCAAAACACACAGAAATATATTCATGTCTAT
GTGTATATAGATCAAAATGTTTTTTTTTGGTATATATAACCCAGGTACACCAGAGC
TTACATATGTTTGAGTTAGACTCTTAAAAATCCTTTGCCAAAAATAAGGGATGGT
CAAATATATGAAACATGTCTTTAGAAAATTTAGGAGATAAAATTTATTTTAA
TTTTGAAACACAAAACAATTTGAATCTTGCTCTCTTAAAGAAAGCATCTTGT
ATATTA AAAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTG (SEQ
ID NO:50)



Figure 2A

1 CTAATAAATATGTTCTCTACACCAAGGCTCATTAAATATTT
46 TAAATATTATATACATTTCTTCTGTGAGAAATACATAAACTTT
91 ATTATATCAGCGCAGGGCGGCGCGGCTCGGTCCCGGAGCAGAA
136 CCCGGCTTTTCTTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA

181 AATGCAACCGGCTCATCTTTGTCTACACTCTAATCTGGCAGAACTT
MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe
226 TTGCACTGTGCGGACACTTCTGCAACCCCGCAGAGCGCATCCAT
CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle
271 CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis
316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGTGAAAGG
LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly
361 AAACGGCTACGTCCAGAGTCTTAGATTCCCGAACAGCTACCCAG
AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg
406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAAATACAG
AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg
451 GATACAGCTAGTGTITGACAATCAGTTTGGATTAGAGGAACAGAG
IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu
496 AAATGATATCTGTAGGTATGATTTTGTGGAGTTGAAGATATATC
AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer
541 CGAAACCACTACCATTTATTAGAGACGATGTTGTGACACAAAGGA
GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu
586 AGTTCTCTCAAGGATAAAATCAAGAACCAACCAATTAATATCAC
ValProProArgIleLysSerArgThrAsnGlnIleLysIleThr
631 ATTCAAGTCGGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT



Figure 2B

PhelLysSerAspAspTyrPheValAlaLysProGlyPheLysIle

5 676 TTATTATTCTTTGCTGGAAGATTTCACCCGAGCAGCTTCAGA
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu

721 GACCAACTGGGAATCTGTACAGCTCTATTTCAGGGTATCCTA
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

10 766 TAACTCTCCATCAGTAACGGATCCCATCTGATTGCGGATGCTCT
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAATTGCAGAAATTGATACAGTGGAGATCTGCTCAA
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

15 856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAAATATGTA
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

901 TCTGGACACCCCTCGGTATCGAGGCAAGTCATACCATGACCGAA
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

20 946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCOTTA
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

991 CAGTTGCACCTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
25 SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCCAAATGTGGTCTTCTTTCCAGTTGCTCTCTCGTGCA
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

30 1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCACTGGAGGTC
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCACATCCAATTCAAGGAAAAACCGTAAAAAGTATCATGAGGT
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

35 1171 ATTACAGTTTGAGCCTGCGCACATCAAGAGGAGGGGTAGAGCTAA
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys



Figure 2C

1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

5 1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

1306 CATCCTTACATTAAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTG
1351 AGATAAGAGACCCCTTTTCCTACCAGCAACCAACTTACTACTAGC
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT
10 1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTTCTAT
1486 ACCTAAGAATATAGGATTGCATTTAATAATAGTGTTTGAGGTTAT
1531 ATATGCACAAACACACACAGAAATATATTTCATGTCTATGTGTATA
1576 TAGATCAAATGTTTTTTTGGTATATATAACCAAGGTACACCAGAG
1621 CTTACATATGTTTGAGTTAGACTCTTAAATCCTTTGGCCAAAATA
15 1666 AGGGATGGTCAAATATATGAAACATGTCTTTAGAAAATTTAGGAG
1711 ATAAATTTATTTTAAATTTTGAACACAAAACAATTTGAATCT
1756 TGCTCTCTTAAAGAAAGCATCTTGTATATTAATAATCAAAAGATG
1801 AGGCTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)



FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCCAT
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTTG
GGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

EVQLVESGGGLVKPGGSLRLSCAASGTFNFRITYNMNVWRQAPGKLEWVSSISS
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIIAS
FYFDYWGGQTLVTVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TTTCAGCAGAAACAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGWFQKPKGKPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHSNYPITFGGGTKVEIK (SEQ
ID NO:14)



FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC
TGAGACTCTCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTATA
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTCAACCATCTC
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCCGTGATTACTGTGCGGGAACGGTGACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

EVQLVQSGGGLIQPGSLRLSCAASGFTVSSNYMSWVRQAPGKLEWVSVIYSG
GSTYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAGTVITNYYYGM
DVWGQGTITVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCC
GGCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCAAAGTAATGGATAC
AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCA GTGGCAGT
GGATCAGGCACAGATTTTACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCTCACTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPRDRFSGSGSDFTLKISRVEAEDVGVYYCMQALQTLTFGGGTKVEI
K (SEQ ID NO:16)



FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC
 TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
 TGGGTCCGCCAGGCTCCAGGCAAGGGGGTGGAGTGGGTGGCAGTTATATGGT
 ATGATGGAAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCCAT
 CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGA
 GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG
 CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
 CACCGTCTCCTCAG (SEQ ID NO:59)

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVIW
 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQGYRYA
 GYYDYDGMDVWGQGTVTVSS (SEQ ID NO:17)

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
 AGTCACCATCACTTGCCGGGCAAGTCAGGCGATTAGAAATGATTAGGCTGG
 TATCAGCAGAAAACAGGGAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
 GTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGGAGTGGATCTGGGACAGA
 ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT
 GTCTACAGCATAATAGTTACCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
 GATCAAAC (SEQ ID NO:60)

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQQKPKAPKRLIYAASSLQ
 SGVPSRFSGSGSTEFTLTISLQPEDFATYYCLQHSYPLTFGGGTKEIK (SEQ
 ID NO:18)



FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCAAACAGTGGTAACACAGGCTATGCACAGAAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC
TGGGACATACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDAVYYCAREGLAVAG
TYYYYYGMDVWGQGTITVTVSS (SEQ ID NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAAACAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTATTCT
GTCTACAGCATAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:62)

D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGRVTITCRASQGIRNDLGWYQQKPKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
ID NO:20)



FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAAGTTCCAGGGCAGAGTCACCA
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG
GGGGAGTTATCGTGCCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDVMITFG
GVIVHYGMDVWGQGTITVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCAACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAAACAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTGACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVDRVTITCRASQGIKNDLQWYQKPGKAPKRLIYAASLQ
SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFQGQTKLEIR (SEQ
ID NO:22)



FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTACCA
TCTCAGCCGACAAGTCCATCAGCACC GCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGHYPG
DSDTRYSPSFQGGVTVISADKSISTAYLQWSSLKASDTAMYICARHVSYYVSGS
YYNVFDYWGQGLVTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGATACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAACGTGGGGTCCCATCAAGGTTACGCGGCAAGTGGATCTGGGACAGA
ATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAA (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQIPGKAPKRLIYAASSLQR
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:24)



FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTATGTGCGAGAGATCAGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:67)

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQGYSG
YVYYDYGMDVWQGTTTVVSS (SEQ ID NO:25)

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
GTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTCCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:68)

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTITCRASQGIKNDLWYQQKPKAPKRLIYAASSLQ
SGVPSRFSGSGSTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKEIK (SEQ
ID NO:26)

**FIGURE 10**

A -- Cur2 1.25.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACC GCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG
GTTCCGAGACTTATTATAATGTCTTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGHIYPG
DSDTRYSPSFQGVITISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSET
YYNVFDYWGQGLTVTVSS (SEQ ID NO:27)

C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCAACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)

D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:28)



FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAAGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCC GGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGCCACCA
TCTCAGCCGACAAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT
ACGATTGGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKSGSYSFSTYWGIVWRQMPGKGLEWMGIYYPG
DSDTRYSPSFQQATISADKSISTAYLQWSSLKASDTAMYICARHVDVIGATIGG
YYYYYHGMVDVWVGQGTITVTVSS (SEQ ID NO:29)

C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCA CTCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCTGATC
TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

D -- Cur2 1.29 light chain protein sequence

DIVMTQSPSLSPVTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPRFSGSGSDFTLTKISRVEADDVGVVYCMQALQSLMCSFGQGTKL
EIK (SEQ ID NO:30)



ANTIBODY DIRECTED TO PDGFD AND USES THEREOF

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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

CAGGTTACAGTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCAC
GGTACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTAYMELRSLRSDDTAVYYCARDHYDSS
DYLYYYYGLDVWGQTTTVVSS (SEQ ID NO:31)

C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAAGTATAACAGTGCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQKPKGVKLLIYAASLTQ
SGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYNAPLTFGGGTKVEIK (SEQ
ID NO:32)



FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTACCGT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIWY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYDSS
DYLYYYYGMDVWVGQTTVTVSS (SEQ ID NO:33)

C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGGTCCTCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT
TCTCTCTACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAAGTGTAACAGTGGCCCGTGGACGTTTCGGCCAAGGGACCACGGTGGAG
ATCAAAAC (SEQ ID NO:76)

D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQQKPKGVPNLLIYAASLTQ
SGVPSRFGSGSGTDFSLTISSLQPEDVAAYYCQKCNAPWTFGQGTVEIK (SEQ
ID NO:34)



FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGCGGAACAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCTGTAAAGGTTCTGGATACAGGTTTACCAGTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA
ATTCCGGGAGTTATTATAACGCTCTTGACTACTGGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGGVITISADKSISTAYLQWSSLKASDTAMYYCARHGSYYNNGS
YYNVFDYWGQGLTVTVSS (SEQ ID NO:35)

C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:78)

D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHSNYPWTFGQGKTEIK (SEQ
ID NO:36)



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FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCCTAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTA VYYCARDIVVVV
AATNYYNGMDVWGQGT VTVSS (SEQ ID NO:37)



FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCACGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGGTTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAIVYYCARGSGYSY
YDYYYGMDVWVGQTTVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGGCGAGTCAGGGCATTAGCAATGATTAGCCTGG
TATCAGCAGAAACCAAGGAAAGTTCTAAGCTCCTGATCTATGCTGCATCCA
CTTTGCAATTAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAACAGTGCCTCCCATTCATTTCCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

DIQMTQSPSSLSASVGDRTINCRASQGISNDLAWYQQKPGKVPKLLIYAASLTQ
LGVPSTRFSGSGSTDFLTITSSLQPEDVATYYCQKYNAPFTFGPGTKVDIK (SEQ
ID NO:39)



FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTCACCAATTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAAATGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCASGYSFTSYDINWVRQATGQGLEWMGWM
NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT
ATDYYYGMDVWGGQTTTVVSS (SEQ ID NO:40)

C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATTTTGCTGCATCCA
GTTTGCCAAGTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAGTGTTACCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTITCRASQGI RNDLGWYQQKPKAPKRLIFAASSLPS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID
NO:41)



FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

CAGGTTACAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAACTATGCACAGAAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQLQGRVTMTTDTSTAYMELRSLRSDDTAVYYCARDVEYYYD
GSGYYYFDYWGQGLVTVSS (SEQ ID NO:42)

C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA
TTTTGCAAAAGTGGGGTCCCATCAAGGTTACAGCGCAGTGGATCTGGGACAGA
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTGCATCTTACTATT
GTCAACAGTCTAACAGTTCCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRTITCRASQGISSWLAWYQQKPKAPKLLIYAASILQ
SGVPSRFSGSGSGTDFTLTISLQPEDFASYYCQQSNSFPRFTFGQGTKVEIK (SEQ
ID NO:43)



FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTGACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTCTGTGCGAGAATGAGGGATATAGTGGC
TACGAGCTATTACTACTTCTACGGTATGGACGTCTGGGGCCAAGGGACC
ACGGTCAACCTGTCTCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDATVYFCARMRDIVAT
SYYYFYFGMDVWVGQTTVTVSS (SEQ ID NO:44)

C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGTCTCTGATC
TATTTGGGTTCTAGTCGGGCCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACCTCTACAACTATCACCTTCGGCCAAGGGA
CACGACTGGAGATTAAAC (SEQ ID NO:87)

D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLHSHNGYNYLDWYLLKPGQSPQLLIYLG
SSRASGVPRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQTITFGQGRLEIK
(SEQ ID NO:45)



FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCTCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGCCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATGCCAAATACAGCCCGTCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTTGA
GGAATTATCGGTATACAGGGTGGTTCGACCCCTGGGGCCAGGGAACCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDAKYSPSFQGGVITISADKSISTAYLQWSSLKASDTAMYCARHYDVWRNY
RYTGWFDPWQGTLVTVSS (SEQ ID NO:46)

C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAT
CCAACAGGGCCACTGGCATCCAGACAGGTTCAGTGGCAGTGGGTCTGGGAC
AGACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTGCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTTCGGCCCTGGGACCAAAGTG
GATATCAAAC (SEQ ID NO:89)

D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLTFTPGTKVDIK (SEQ
ID NO:47)



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FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATAAAC
CCTAATAGTGGTAACACAGACTATGCACAGAAAGTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTTGGATACAGCTAT
AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

QVQLVQSGAEVKKPGASVKVSCKASGYFTFSYDINWVRQATGQGLEWMGWIN
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYYYGMDVWGQGTTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAAGGCCAGTCAGAGTGTTAGTAGTAGTTACTTAGCCT
GGTACCAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGCCACTGGCATCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTGCAGTGATTA
CTGTGACGAGTATGGTAGTTCACCGTGCAGTTTGGCCAGGGGACCAAGCTG
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPSFSGQGTKLEIK (SEQ
ID NO:49)



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FIGURE 22A

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4	
CR2							V					D & J
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0	
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0	0/0
	VK	mix										
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0



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FIGURE 22B

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	CR2						V			D & J	
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0

**FIGURE 23****Figure 23A**

	(1)	1	10	20	30	40	51	Section 1
CUR2-1.61 HC	(1)	EVQLVESGGGLVKP	GGSLRLSCAASG	FNER	YNNHWVRQAPG	KGLEWVSSI		
VH3-21	(1)	EVQLVESGGGLVKP	GGSLRLSCAASG	FTFSS	YNNHWVRQAPG	KGLEWVSSI		
Consensus	(1)	EVQLVESGGGLVKP	GGSLRLSCAASG	F SY	MNNWVRQAPG	KGLEWVSSI		
	(62)	52	60	70	80	90	102	Section 2
CUR2-1.61 HC	(62)	SSSSSNLYKADSVK	GFRTISRDNKNS	SLVLMNSLRAD	TAHYVCARDMI			
VH3-21	(62)	SSSSSNLYKADSVK	GFRTISRDNKNS	SLVLMNSLRAD	TAHYVCAR----			
Consensus	(62)	SSSSS IYYADSVK	GFRTISRDNKNS	SLVLMNSLRAD	TAHYVCAR			
	(103)	103	110	126				Section 3
CUR2-1.61 HC	(103)	TFGGIIASFPDY	WGQSTLVTVSS					
VH3-21	(89)	-----						
Consensus	(103)							

Figure 23B

	(1)	1	10	20	30	40	51	Section 1
CUR2-1.61 LC	(1)	DIQMTQSPSSLSAS	VGDRVITCRASQ	GIRNDLGM	QKQKPKAPRLI	YAA		
A30	(1)	DIQMTQSPSSLSAS	VGDRVITCRASQ	GIRNDLGM	QKQKPKAPRLI	YAA		
Consensus	(1)	DIQMTQSPSSLSAS	VGDRVITCRASQ	GIRNDLGM	QKQKPKAPRLI	YAA		
	(62)	52	60	70	80	90	102	Section 2
CUR2-1.61 LC	(62)	SSLCQGVPSRPS	SGSGGTETLTIS	SLQPEDFATYYC	LQHNNSYP	ELTPGGGT		
A30	(62)	SSLCQGVPSRPS	SGSGGTETLTIS	SLQPEDFATYYC	LQHNNSYP	ELTPGGGT		
Consensus	(62)	SSLCQGVPSRPS	SGSGGTETLTIS	SLQPEDFATYYC	LQHNNSYP			
	(103)	103	107					Section 3
CUR2-1.61 LC	(103)	KVEIK						
A30	(86)	-----						
Consensus	(103)							

Figure 24A

	(1)	10	20	30	40	51	Section 1
Cu2-1.11.1 HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWRQAPGKGLWVSI					
VH-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWRQAPGKGLWVSI					
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWRQAPGKGLWVSI					
	(52)	52	60	70	80	90	102
Cu2-1.11.1 HC	(52)	YSGGSTYYADSVKRGFTISRDNSENKTYLQMNLSRAEDTAVYYCA					
VH-53	(52)	YSGGSTYYADSVKRGFTISRDNSENKTYLQMNLSRAEDTAVYYCA					
Consensus	(52)	YSGGSTYYADSVKRGFTISRDNSENKTYLQMNLSRAEDTAVYYCA					
	(103)	103	110	120			Section 3
Cu2-1.11.1 HC	(103)	YYYGGDVMGGSGTFTVSS					
VH-53	(96)	-----					
Consensus	(103)	-----					

Figure 24B

Section 1

(1) 1 10 20 30 40 51

CUR2-1.11.1_LC A19 (1) DIVMTQSPFISLPVTPGEPASIFCRSSQSLHSNGVNYLDWYLRQPGQSPQL

Consensus (1) DIVMTQSPFISLPVTPGEPASIFCRSSQSLHSNGVNYLDWYLRQPGQSPQL

Section 2

(52) 52 60 70 80 90 102

CUR2-1.11.1_LC A19 (52) LYLIGSNRASPVGVDPRPSSGSGSTDPFLKISRVEADVGYYVYCMQALQTLFP

Consensus (52) LYLIGSNRASPVGVDPRPSSGSGSTDPFLKISRVEADVGYYVYCMQALQTFP

Section 3

(103) 103 111

CUR2-1.11.1_LC A19 (103) GGGTKVIEIK

Consensus (103) -----

FIGURE 25**Figure 25A**

	(1)	10	20	30	40	51	Section 1
CR2-1.17.1 HC	(1)	QVQLVSEGGGVVQPG	SRISCAASGPTT	SSYGMHWVRQAP	FGKGLEWVAVI		
VH3-33	(1)	QVQLVSEGGGVVQPG	SRISCAASGPTT	SSYGMHWVRQAP	FGKGLEWVAVI		
Consensus	(1)	QVQLVSEGGGVVQPG	SRISCAASGPTT	SSYGMHWVRQAP	FGKGLEWVAVI		
	(52)	60	70	80	90	102	Section 2
CR2-1.17.1 HC	(52)	WYDGSNKYYADSVKGRPT	ISRDSRNNTLYIQNS	LRAEDTAVYYCAR	DQGY		
VH3-33	(52)	WYDGSNKYYADSVKGRPT	ISRDSRNNTLYIQNS	LRAEDTAVYYCAR	---		
Consensus	(52)	WYDGSNKYYADSVKGRPT	ISRDSRNNTLYIQNS	LRAEDTAVYYCAR	---		
	(103)	110	126				Section 3
CR2-1.17.1 HC	(103)	RYAGYYVDYGM	VMGGTTVTVS				
VH3-33	(99)	-----					
Consensus	(103)						

Figure 25B

	(1)	10	20	30	40	52	Section 1
CR2-1.17.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGITRNDL	GWYQKPKGKAPKRLIYAAS				
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGITRNDL	GWYQKPKGKAPKRLIYAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGITRNDL	GWYQKPKGKAPKRLIYAAS				
	(53)	60	70	80	90	104	Section 2
CR2-1.17.1 LC	(53)	SLQSGVPFRFSGSGSGTEFTLTISSDQPEDPATYYC	QHNWYFELTPGGGTKV				
A30	(53)	SLQSGVPFRFSGSGSGTEFTLTISSDQPEDPATYYC	QHNWYFELTPGGGTKV				
Consensus	(53)	SLQSGVPFRFSGSGSGTEFTLTISSDQPEDPATYYC	QHNWYFELTPGGGTKV				
	(105)	1067					Section 3
CR2-1.17.1 LC	(105)	BIK					
A30	(96)	---					
Consensus	(105)						

FIGURE 26

Figure 26A

	(1)	10	20	30	40	50	Section 1
CR2-118_HC	(1)	QVQLVQSGAEVVKRPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMHGHN					
VH1-8	(1)	QVQLVQSGAEVVKRPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMHGHN					
Consensus	(1)	QVQLVQSGAEVVKRPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMHGHN					
	(53)	60	70	80	90	104	Section 2
CR2-118_HC	(53)	PNESGTYGAQRFGQGRVTMTNRTSISTAYMELSSLSASEDTAVVYCAREGTAAV					
VH1-8	(53)	PNESGTYGAQRFGQGRVTMTNRTSISTAYMELSSLSASEDTAVVYCAREGTAAV					
Consensus	(53)	PNESGTYGAQRFGQGRVTMTNRTSISTAYMELSSLSASEDTAVVYCAREGTAAV					
	(105)	105	110	126			Section 3
CR2-118_HC	(105)	GTYYTYYGMDVWGEGGTFTVSS					
VH1-8	(99)	-----					
Consensus	(105)	-----					

Figure 26B

	(1)	10	20	30	40	Section 1
CR2-1.18 LC	(1)	DIQMTQSPPSLSASVGRVIT	TCRA	SGQGINRDLGWYQOKPGKAPKRLIYAAS		53
A30	(1)	DIQMTQSPPSLSASVGRVIT	TCRA	SGQGINRDLGWYQOKPGKAPKRLIYAAS		
Consensus	(1)	DIQMTQSPPSLSASVGRVIT	TCRA	SGQGINRDLGWYQOKPGKAPKRLIYAAS		
	(54)	54	60	70	80	90
CR2-1.18 LC	(54)	LOGSVFSAFSSGGSGTEFTL	TISSLOLPEDPATY	CLQHN	SYPTTFPGTGKVI	106
A30	(54)	LOGSVFSAFSSGGSGTEFTL	TISSLOLPEDPATY	CLQHN	SYPTTFPGTGKVI	
Consensus	(54)	LOGSVFSAFSSGGSGTEFTL	TISSLOLPEDPATY	CLQHN	SYPTTFPGTGKVI	
	(107)	107				Section 3
CR2-1.18 LC	(107)	K				
A30	(66)	K				
Consensus	(107)	K				

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FIGURE 27

Figure 27A

Section 1						
	(1)	10	20	30	40 52	
Cu2-1.19.1_hc	(1)	QVQLVQSGAEVKKRPGASVKVSCKASGYTFSTSYDINWVRQATGGQGLEWVGMMN				
VH1-6	(1)	QVQLVQSGAEVKKRPGASVKVSCKASGYTFSTSYDINWVRQATGGQGLEWVGMMN				
Consensus	(1)	QVQLVQSGAEVKKRPGASVKVSCKASGYTFSTSYDINWVRQATGGQGLEWVGMMN				
Section 2						
	(53)	60	70	80	90 104	
Cu2-1.19.1_hc	(53)	FNSGNTGYAKFQGRVTMTNTSISTAYMELSSLASEDTAVYYCARDVMTF				
VH1-6	(53)	FNSGNTGYAKFQGRVTMTNTSISTAYMELSSLASEDTAVYYCAR-----				
Consensus	(53)	FNSGNTGYAKFQGRVTMTNTSISTAYMELSSLASEDTAVYYCAR				
Section 3						
	(105)	110	126			
Cu2-1.19.1_hc	(105)	GGVIVHYGMDVMGQGTTVTVSS				
VH1-6	(99)	-----				
Consensus	(105)					

Figure 27B

Section 1						
	(1)	10	20	30	40 52	
Cu2-1.19.1 Ic	(1)	DIQMTQSFSSLSASVGDRTVITTCRASQGIANDLWYQKRPAPRLIYAAS				
A30	(1)	DIQMTQSFSSLSASVGDRTVITTCRASQGIANDLWYQKRPAPRLIYAAS				
Consensus	(1)	DIQMTQSFSSLSASVGDRTVITTCRASQGIANDLWYQKRPAPRLIYAAS				
Section 2						
	(53)	60	70	80	90 104	
Cu2-1.19.1 Ic	(53)	SLQSGVPSKRPSSGSGSTFTLTISSLQPEDFATYYCLQHNSEFCFQGQTRL				
A30	(53)	SLQSGVPSKRPSSGSGSTFTLTISSLQPEDFATYYCLQHNSEFCFQGQTRL				
Consensus	(53)	SLQSGVPSKRPSSGSGSTFTLTISSLQPEDFATYYCLQHNSEFCFQGQTRL				
Section 3						
	(105)	106				
Cu2-1.19.1 Ic	(105)	EIR				
A30	(96)	---				
Consensus	(105)					



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FIGURE 28

Figure 28A

Section 1					
	(1)	10	20	30	40
Cur2-1.23.1_HC	(1)	EVQLVQSGAEVKKRQEGGSLRTECSGGSGVSRFTSYWIGWVLRMPGKGLNWMGII			
VH5-51	(1)	EVQLVQSGAEVKKRQEGGSLRTECSGGSGVSRFTSYWIGWVLRMPGKGLNWMGII			
Consensus	(1)	EVQLVQSGAEVKKRQEGGSLRTECSGGSGVSRFTSYWIGWVLRMPGKGLNWMGII			
Section 2					
	(52)	62	70	80	90
Cur2-1.23.1_HC	(52)	YFGDSDFYSPFQGGVTISADKSTSTAYLQNSSLKASDTAMYTCARHVS			
VH5-51	(52)	YFGDSDFYSPFQGGVTISADKSTSTAYLQNSSLKASDTAMYTCARHVS			
Consensus	(52)	YFGDSDFYSPFQGGVTISADKSTSTAYLQNSSLKASDTAMYTCARHVS			
Section 3					
	(103)	103	110	126	
Cur2-1.23.1_HC	(103)	YYVSGSYYNVFDYWGQGLVTVSS			
VH5-51	(99)	-----			
Consensus	(103)	-----			

Figure 28B

Section 1					
	(1)	10	20	30	40
Cur2-1.23.1_LC	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGSWYQQIFPKAPKRLIYAA			
A30	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGSWYQQIFPKAPKRLIYAA			
Consensus	(1)	DIQMTQSPFSSLSASVGDRTITCRASQGISIRNDLGSWYQQIFPKAPKRLIYAA			
Section 2					
	(52)	62	70	80	90
Cur2-1.23.1_LC	(52)	SSLQSGVSRFRFGSGSGTEFTLTISSLQPEDFATYYCLOHNSYFPGGT			
A30	(52)	SSLQSGVSRFRFGSGSGTEFTLTISSLQPEDFATYYCLOHNSYFPGGT			
Consensus	(52)	SSLQSGVSRFRFGSGSGTEFTLTISSLQPEDFATYYCLOHNSYFPGGT			
Section 3					
	(103)	103	107		
Cur2-1.23.1_LC	(103)	KVEIK			
A30	(96)	-----			
Consensus	(103)	-----			



FIGURE 29

Figure 29A

						Section 1
						10 20 30 40 51
CR2-1.24.1_HC	(1)	OVQLVBSGCGVVPQGRSLRLSCAASG				PSYGMHWVQAQPGKGLEWADI
WG-33	(1)	OVQLVBSGGGVVPQGRSLRLSCAASG				PSYGMHWVQAQPGKGLEWVAUT
Consensus	(1)	OVQLVBSGGGVVPQGRSLRLSCAASG				PSYGMHWVQAQPGKGLEWVA I
						Section 2
						(52) 52 60 70 80 90 102
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAETAVYYCARDQGY				
WG-33	(52)	WYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAETAVYYCAR				
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAETAVYYCAR				
						Section 3
						(103) 103 110 126
CR2-1.24.1_HC	(103)	SYGYVYYDYGMDVWGQSTTVTVSS				
WG-33	(99)	-----				
Consensus	(103)					

Figure 29B

						Section 1
						(1) 1 10 20 30 40 52
CR2-1.24.1_LC	(1)	DIQMTQSPDSLSASVGDRVTITCRASQGIIRNDLGWYQQKPKGKAPKRLIYAAS				
A30	(1)	DIQMTQSPDSLSASVGDRVTITCRASQGIIRNDLGWYQQKPKGKAPKRLIYAAS				
Consensus	(1)	DIQMTQSPDSLSASVGDRVTITCRASQGIIRNDLGWYQQKPKGKAPKRLIYAAS				
						Section 2
						(53) 53 60 70 80 90 104
CR2-1.24.1_LC	(53)	SIQSGVPSRFSGSGSGTEFTLTISLPQPEDPATYYCLQHNSTYFPQGTQKVF				
A30	(53)	SIQSGVPSRFSGSGSGTEFTLTISLPQPEDPATYYCLQHNSTYFP-----				
Consensus	(53)	SIQSGVPSRFSGSGSGTEFTLTISLPQPEDPATYYCLQHNSTYFP				
						Section 3
						(105) 1057
CR2-1.24.1_LC	(105)	RIK				
A30	(96)	---				
Consensus	(105)					



FIGURE 30

Figure 30A

		Section 1				
	(1)	1	10	20	30	40
VH5-51	(1)	EVQLVQSGAEVRRGDSGEEKISCKNGSCYSFTSYWIGWVRQMPFGKLEWNGII				51
CR2-1.25.1_HC	(1)	EVQVQSGAEVKKFQDSGKLISCKNGSCYSFTSYWIGWVRQMPFGKLEWNGII				
Consensus	(1)	EVQLVQSGAEVKKFQDSGKLISCKNGSGY	FTSYWIGWVRQMPFGKLEWNGII			
		Section 2				
	(52)	52	60	70	80	90
VH5-51	(52)	YFGDSDDTRYSPFQSGQVTISADKSIISTAYLQWSSSLKASDTAMYYCAR---				102
CR2-1.25.1_HC	(52)	YFGDSDDTRYSPFQSGQVTISADKSIISTAYLQWSSSLKASDTAMYYCARHGSY				
Consensus	(52)	YFGDSDDTRYSPFQSGQVTISADKSIISTAYLQWSSSLKASDTAMYYCAR				
		Section 3				
	(103)	103	110	126		
VH5-51	(99)	-----				
CR2-1.25.1_HC	(103)	YYGSETYYNVFDYWGQGLTVTS8				
Consensus	(103)					

Figure 30B

		Section 1				
	(1)	1	10	20	30	40
A30	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKAPRRLLIYAAS				52
CR2-1.25.1_LC	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKAPRRLLIYAAS				
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQKPKGKAPRRLLIYAAS				
		Section 2				
	(53)	53	60	70	80	90
A30	(53)	SLQSGVFPSPFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP-----				104
CR2-1.25.1_LC	(53)	SLQSGVFPSPFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYEWTPFGQGTKV				
Consensus	(53)	SLQSGVFPSPFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP				
		Section 3				
	(105)	105	107			
A30	(96)	---				
CR2-1.25.1_LC	(105)	EIK				
Consensus	(105)					



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FIGURE 31

Figure 31A

Section 1					
	(1)	10	20	30	40 52
VH5-51	(1)	EVQLVQSGAEVKKRPGESLKI	ISCKGSGVSTFSLWIGGVVRQMP	PGRGLEMMGIIV	
CR2-1.29_HC	(1)	EVQLVQSGAEVKKRPGESLKI	ISCKGSGVSTFSLWIGGVVRQMP	PGRGLEMMGIIV	
Consensus	(1)	EVQLVQSGAEVKKRPGESLKI	ISCKGSGVSTFSLWIGGVVRQMP	PGRGLEMMGIIV	
Section 2					
	(53)	60	70	80	90 104
VH5-51	(53)	EGDSDTRYSPFQGGQVIT	ISADKSIISTAYLQWSS	LKASDTAMYYCAR	-----
CR2-1.29_HC	(53)	EGDSDTRYSPFQGGQVIT	ISADKSIISTAYLQWSS	LKASDTAMYYCAR	HVDVGA
Consensus	(53)	EGDSDTRYSPFQGGQ	TISADKSIISTAYLQWSS	LKASDTAMYYCAR	
Section 3					
	(105)	106	110	129	
VH5-51	(99)	-----	-----	-----	
CR2-1.29_HC	(105)	TIGGYYYYHGM	DVMGGGT	TVTVSS	
Consensus	(105)				

Figure 31B

Section 1					
	(1)	10	20	30	40 53
A19	(1)	DI VMTQSPFLSLPVTGPE	PAISCRSSQSLHNGYNYL	WDYLQKPGQSP	QLLI
CR2-1.29_LC	(1)	DI VMTQSPFLSLPVTGPE	PAISCRSSQSLHNGYNYL	WDYLQKPGQSP	QLLI
Consensus	(1)	DI VMTQSPFLSLPVTGPE	PAISCRSSQSLHNGYNYL	WDYLQKPGQSP	QLLI
Section 2					
	(54)	60	70	80	90 106
A19	(54)	YLGSNRAHGVPDRFSGSG	SGTDFTLKISRVEA	LDVGVYYCMQAL	LP-----
CR2-1.29_LC	(54)	YLGSNRAHGVPDRFSGSG	SGTDFTLKISRVEA	LDVGVYYCMQAL	LMCSFGQ
Consensus	(54)	YLGSNRAHGVPDRFSGSG	SGTDFTLKISRVEA	LDVGVYYCMQAL	QS
Section 3					
	(107)	107	113		
A19	(101)	-----	-----		
CR2-1.29_LC	(107)	GTKLEIK			
Consensus	(107)				



FIGURE 32

Figure 32A

						Section 1
						52
VH1-18	(1)	10	20	30	40	
CR2-1.33_HC	(1)	QVQLVQSGAEVRRPGASVVKVSCRASGYTFPSVGI	SWVRQAPGGGLEMMGWIS			
Consensus	(1)	QVQLVQSGAEVRRPGASVVKVSCRASGYTFPSYGI	SWVRQAPGGGLEMMGWIS			
						Section 2
						104
VH1-18	(53)	53	60	70	80	
CR2-1.33_HC	(53)	AYNGNTNYAQLQGRVTMTTDTSTSTAYMELASLRSDDTAVYYCAR				
Consensus	(53)	AYNGNTNYAQLQGRVTMTTDTSTSTAYMELASLRSDDTAVYYCAR				
						Section 3
						127
VH1-18	(105)	105	110			
CR2-1.33_HC	(105)	SDYLYYYVGLDVMGGSTTVTVSS				
Consensus	(105)					

Figure 32B

						Section 1
						53
A20	(1)	10	20	30	40	
CR2-1.33_LC	(1)	DIQWTQSPSSLSASVGRVITICRASQGISNYLAWYQQRPGKVPRLITVAAST				
Consensus	(1)	DIQWTQSPSSLSASVGRVITICRASQGISNYLAWYQQRPGKVPRLITVAAST				
						Section 2
						106
A20	(54)	54	60	70	80	
CR2-1.33_LC	(54)	IQSGVPSRFSGSGSGTDFTLTISGLQPEDVATYYCKYNSAP				
Consensus	(54)	IQSGVPSRFSGSGSGTDFTLTISGLQPEDVATYYCKYNSAP				
						Section 3
						107
A20	(107)	107				
CR2-1.33_LC	(107)	K				
Consensus	(107)					

FIGURE 33

Figure 33A

	(1)	10	20	30	40	51	Section 1
VH3-33	(1)	QVQLVDSGGGVVQPGRLRLSCAASGTFSSYGNHWRVQAGKGLNVAWT					
CR2-1.38.1_HC	(1)	QVQLVDSGGGVVQPGRLRLSCAASGTFSSYGNHWRVQAGKGLNVAWT					
Consensus	(1)	QVQLVDSGGGVVQPGRLRLSCAASGTFSSYGNHWRVQAGKGLNVAWT					
	(52)	52	60	70	80	90	102
VH3-33	(52)	YDGNKRYKADSVKGRFTISRDNEKNTLYLQNMRSLAEATVYYCAR					
CR2-1.38.1_HC	(52)	YDGNKRYKADSVKGRFTISRDNEKNTLYLQNMRSLAEATVYYCAR					
Consensus	(52)	YDGNKRYKADSVKGRFTISRDNEKNTLYLQNMRSLAEATVYYCAR					
	(103)	103	110	127			Section 3
VH3-33	(98)	-----					
CR2-1.38.1_HC	(103)	DSDDYLYYYGVDMVGQETTIVSS					
Consensus	(103)	-----					

Figure 33B

Section 1
 A20 (1) DTQMTGSPFSLASVGDVRVITTCRASGGISNYLAWQQKQKPGKPVLLIYAAS 52
 CR2.138.1_LC (1) DTQMTGSPFSLASVGDVRVITTCRASGGISNYLAWQQKQKPGKPVLLIYAAS
 Consensus (1) DTQMTGSPFSLASVGDVRVITTCRASGGISNYLAWQQKQKPGKPV LLIYAAS
 Section 2
 A20 (53) 53 60 70 80 90 104
 CR2.138.1_LC (53) TLQSGVPRFRSFGSGSGTDFSLTISSLQPELVATYYQKYNBSAF
 Consensus (53) TLQSGVPRFRSFGSGSGTDFSLTISSLQPELVAA YYCQK NBSAF
 Section 3
 A20 (105) 1067
 CR2.138.1_LC (105) EIK
 Consensus (105)

FIGURE 34

Figure 34A

	(1)	1	10	20	30	40	51	Section 1
VH5-51	(1)	EVQLVQSGAEVVRKPEGSERISCKGSGVSPTSYMIGWVRQMPGKGLRWGGII						
CR2-1.39.1_HC	(1)	EVQLVQSGTEVVRKPEGSERISCKGSGVSPTSYMIGWVRQMPGKGLRWGGII						
Consensus	(1)	EVQLVQSG EVVRKPEGSERISCKGSGVSPTSYMIGWVRQMPGKGLRWGGII						
	(52)	52	60	70	80	90	102	Section 2
VH5-51	(52)	YFGDSDDTRYSPSFQGGQVTISADKSIISTAYLQWSSLKASDTAMYVCAR----						
CR2-1.39.1_HC	(52)	YFGDSDDTRYSPSFQGGQVTISADKSIISTAYLQWSSLKASDTAMYVCARHGSY						
Consensus	(52)	YFGDSDDTRYSPSFQGGQVTISADKSIISTAYLQWSSLKASDTAMYVCAR						
	(103)	103	110	126				Section 3
VH5-51	(96)	-----						
CR2-1.39.1_HC	(103)	YYNBSGYYNVFDYWGQGLTVVSS						
Consensus	(103)							

Figure 34B

	(1)	1	10	20	30	40	52	Section 1
A30	(1)	DIQMTQSPFSSLSASVGDVYTCRAAGGIRNDLGWYQKPKGKAPKRLIYAAS						
CR2-1.39.1_LC	(1)	DIQMTQSPFSSLSASVGDVYTCRAAGGIRNDLGWYQKPKGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPFSSLSASVGDVYTCRAAGGIRNDLGWYQKPKGKAPKRLIYAAS						
	(53)	53	60	70	80	90	104	Section 2
A30	(53)	SLQSGVSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP-----						
CR2-1.39.1_LC	(53)	SLQSGVSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYFMTFGQGTKV						
Consensus	(53)	SLQSGVSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP						
	(105)	105	117					Section 3
A30	(96)	---						
CR2-1.39.1_LC	(105)	BIK						
Consensus	(105)							



FIGURE 35

Figure 35A

		Section 1					
	(1)	1	10	20	30	40	52
VH1-8	(1)	QVQLVQSGAEVKRPGASVKVSCFASGYTFSSVDINNVKQATGQGLEWMGWMN					
CR2-1.45_HC	(1)	QVQLVQSGAEVKRPGASVKVSCFASGYTFSSVDINNVKQATGQGLEWMGWMN					
Consensus	(1)	QVQLVQSGAEVKRPGASVKVSCFASGYTFSSVDINNVKQATGQGLEWMGWMN					
		Section 2					
	(53)	53	60	70	80	90	104
VH1-8	(53)	PNSGNTGYACKPGQGVMTNTSTSTAYMELSLRSEDTAVYYCAR-----					
CR2-1.45_HC	(53)	PNSGNTGYACKPGQGVMTNTSTSTAYMELSLRSEDTAVYYCARSGGSGYSY					
Consensus	(53)	PNSGNTGYACKPGQGVMTNTSTSTAYMELSLRSEDTAVYYCAR					
		Section 3					
	(105)	105	110	125			
VH1-8	(99)	-----					
CR2-1.45_HC	(105)	GYDYYGYGMDVMVGQGTTFVTVSS					
Consensus	(105)						

Figure 35B

		Section 1				
	(1)	10	20	30	40	53
A20	(1)	DIQMTQSPFSLRASVGDRTVITCRASQGISNVLAWYQKPKRVKLLIYAAS				
CR2-1.45_LC	(1)	DIQMTQSPFSLRASVGDRTVITCRASQGISNVLAWYQKPKRVKLLIYAAS				
Consensus	(1)	DIQMTQSPFSLRASVGDRTVITCRASQGISNVLAWYQKPKRVKLLIYAAS				
		Section 2				
	(54)	60	70	80	90	106
A20	(54)	LQSGVFSRFRGGSGGTDFTLTISSLQPEDVATYYCQKYNBAP-----				
CR2-1.45_LC	(54)	LQLGVEGDSRGGSGGTDFTLTISSLQPEDVATYYCQKYNBAPFTTTPGPKRVDI				
Consensus	(54)	LQGVFSRFRGGSGGTDFTLTISSLQPEDVATYYCQKYNBAP				
		Section 3				
	(107)	107				
A20	(96)	-				
CR2-1.45_LC	(107)	K				
Consensus	(107)					



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FIGURE 36

Figure 36A

		(1)	1	10	20	30	40	51	Section 1
VH1-8	(1)	QVQLVQSGAEYVKRPGASVKVSKASGY	FTSYDINWVRQATGQGLEWNGWM						
CR2-1.46.1_HC	(1)	QVQLVQSGAEYVKRPGASVKVSKASGY	FTSYDINWVRQATGQGLEWNGWM						
Consensus	(1)	QVQLVQSGAEVKKRPGASVKVSKASGY	FTSYDINWVRQATGQGLEWNGWM						
		(52)	52	60	70	80	90	102	Section 2
VH1-8	(52)	NPNNGNTGYAQRFGSRVTMTNTSISTAYMELSSLRSEDTAVVYCAR	----						
CR2-1.46.1_HC	(52)	NPNNGNTGYAQRFGSRVTMTNTSISTAYMELSSLRSEDTAVVYCAR	----						
Consensus	(52)	NPN GNTGYAQRFGSRVTMTNTSISTAYMELSSLRSEDTAVVYCAR							
		(103)	103	110	126				Section 3
VH1-8	(99)	-----							
CR2-1.46.1_HC	(103)	VVATDYYYGMDVVGQGTTVTVSS							
Consensus	(103)								

Figure 36B

		(1)	1	10	20	30	40	52	Section 1
A30	(1)	DIQMTQSPDSLSASVGRVITCRASGIRNDLQWYQKPKGKAPRLITAAAS							
CR2-1.46.1_LC	(1)	DIQMTQSPDSLSASVGRVITCRASGIRNDLQWYQKPKGKAPRLITAAAS							
Consensus	(1)	DIQMTQSPDSLSASVGRVITCRASGIRNDLQWYQKPKGKAPRLITAAAS							
		(53)	53	60	70	80	90	104	Section 2
A30	(53)	SLSGGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP	-----						
CR2-1.46.1_LC	(53)	SLSGGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP	-----						
Consensus	(53)	SLSGGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP							
		(105)	105	117					Section 3
A30	(96)	---							
CR2-1.46.1_LC	(105)	EIK							
Consensus	(105)								

FIGURE 37

Figure 37A

	Section 1				
	(1)	10	20	30	40
CR2-148.1_HC	(1)	QVQLVQSGAEVRKKPGASV	RVSKASGYTPTSTYGISWVRQAPGGGLEW	MGWI	51
VH1-18	(1)	QVQLVQSGAEVRKKPGASV	RVSKASGYTPTSTYGISWVRQAPGGGLEW	MGWI	
Consensus	(1)	QVQLVQSGAEVRKKPGASV	RVSKASGYTPTSTYGISWVRQAPGGGLEW	MGWI	
	Section 2				
	(52)	60	70	80	90
CR2-148.1_HC	(52)	SAYNGNTNYAQKLGSRVTMTDTSTSTAYMELRSLRBDTAVYYCARDV	Y		102
VH1-18	(52)	SAYNGNTNYAQKLGSRVTMTDTSTSTAYMELRSLRBDTAVYYCAR	---		
Consensus	(52)	SAYNGNTNYAQKLGSRVTMTDTSTSTAYMELRSLRBDTAVYYCAR			
	Section 3				
	(103)	110	125		
CR2-148.1_HC	(103)	YYDGGVYYPDYWGQGLTVTVSS			
VH1-18	(99)	-----			
Consensus	(103)				

Figure 37B

	Section 1				
	(1)	10	20	30	40
CR2-148.1_LC	(1)	DIQMTQSPDSVSAVSDRVITTCRAAGGISWLA	WYQRRPGKAPKLLIYAAS		52
L5	(1)	DIQMTQSPDSVSAVSDRVITTCRAAGGISWLA	WYQRRPGKAPKLLIYAAS		
Consensus	(1)	DIQMTQSPDSVSAVSDRVITTCRAAGGISWLA	WYQRRPGKAPKLLIYAAS		
	Section 2				
	(53)	60	70	80	90
CR2-148.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFA	LYCQQNSFPRTFGGQTKV		104
L5	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFA	LYCQQNSFP-----		
Consensus	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFA	LYCQQNSFP		
	Section 3				
	(105)	1067			
CR2-148.1_LC	(105)	RIK			
L5	(96)	---			
Consensus	(105)				

Figure 38A

Figure 38B

	(1)	10	20	30	40	52	Section 1
CR2-1.49.1_LC	(1)	DIYMTQSLSLFVTPGEPASISCRSSQSLHSHNGYNYDYLXKPGQSPQLL					
A19	(1)	DIYMTQSLSLFVTPGEPASISCRSSQSLHSHNGYNYDYLXKPGQSPQLL					
Consensus	(1)	DIYMTQSLSLFVTPGEPASISCRSSQSLHSHNGYNYDYLXKPGQSPQLL					
	(53)	53	60	70	80	90	104
CR2-1.49.1_LC	(53)	YLIGSSRASGVDFRPSGSGSGDTFLTKISRAVEADVGVYECMOTLIITFFGQ					
A19	(53)	YLIGSSRASGVDFRPSGSGSGDTFLTKISRAVEADVGVYECMOTLIITFFGQ					
Consensus	(53)	YLIGS RASGVDFRPSGSGSGDTFLTKISRAVEADVGVYECMQ LQT					
	(105)	105	111				Section 3
CR2-1.49.1_LC	(105)	STALEK					
A19	(101)	-----					
Consensus	(105)						

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FIGURE 39

Figure 39A

		Section 1				
		(1)	10	20	30	40
CR2-1.51.1 HC	(1)	1	10	20	30	40
VH5-51	(1)	1	10	20	30	40
Consensus	(1)	1	10	20	30	40
		Section 2				
		(52)	52	60	70	80
CR2-1.51.1 HC	(52)	52	60	70	80	90
VH5-51	(52)	52	60	70	80	90
Consensus	(52)	52	60	70	80	90
		Section 3				
		(103)	103	110	126	
CR2-1.51.1 HC	(103)	103	110	126		
VH5-51	(99)	-----				
Consensus	(103)					

Figure 39B

		Section 1					
		(1)	10	20	30	40	52
CR2-1.51.1 LC	(1)	1	10	20	30	40	52
A27	(1)	1	10	20	30	40	52
Consensus	(1)	1	10	20	30	40	52
		Section 2					
		(53)	60	70	80	90	104
CR2-1.51.1 LC	(53)	53	60	70	80	90	104
A27	(53)	53	60	70	80	90	104
Consensus	(53)	53	60	70	80	90	104
		Section 3					
		(105)	108	08			
CR2-1.51.1 LC	(105)	105	108	08			
A27	(97)	---					
Consensus	(105)	105	108	08			

FIGURE 40

Figure 40A

		Section 1				
		(1)	10	20	30	40 52
Cu2-6.4.1 hc	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTFPSYDINWVRQATGQGLEWMGW				
VH1-8	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTFPSYDINWVRQATGQGLEWMGW				
Consensus	(1)	QVQLVQSGAEVKKFGASVKVSCKASGYTFPSYDINWVRQATGQGLEWMGW				
		Section 2				
		(53)	60	70	80	90 104
Cu2-6.4.1 hc	(53)	PNSSNTDYAQNFGGRVTMTPTSTSTAYMBLSSRSBDTA				
VH1-8	(53)	PNSSNTGYACKFQGRVTMTPTSTSTAYMBLSSRSBDTA				
Consensus	(53)	PNSSNT YAQKFGGRVTMTPTSTSTAYMBLSSRSBDTA				
		Section 3				
		(105)	105	110	125	
Cu2-6.4.1 hc	(105)	NYDYVYGHVDVWGQGTPTVTVSS				
VH1-8	(99)	-----				
Consensus	(105)					

Figure 40B

		Section 1				
		(1)	10	20	30	40 52
Cu2-6.4.1 Lc	(1)	EIVLTQSPFTLSLSPGGERATLSCRASQSVSSSYLANWYQKQPGQAPRLIY				
A27	(1)	EIVLTQSPFTLSLSPGGERATLSCRASQSVSSSYLANWYQKQPGQAPRLIY				
Consensus	(1)	EIVLTQSPFTLSLSPGGERATLSCRASQSVSSSYLANWYQKQPGQAPRLIY				
		Section 2				
		(53)	60	70	80	90 104
Cu2-6.4.1 Lc	(53)	SSRATGIPDRFSGSGSTDFLTISRLEPEDFAVYYCQYGSSECFPGQSTK				
A27	(53)	SSRATGIPDRFSGSGSTDFLTISRLEPEDFAVYYCQYGSSECFPGQSTK				
Consensus	(53)	SSRATGIPDRFSGSGSTDFLTISRLEPEDFAVYYCQYGSSECFPGQSTK				
		Section 3				
		(105)	105	109	109	
Cu2-6.4.1 Lc	(105)	LEIK				
A27	(97)	----				
Consensus	(105)					

Figure 41B

1.19. 3	A30	-3	TTACCC (SEQ ID NO:198)	6	GTGCAG (SEQ ID NO:199)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A37/A37A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.2	A37/A37A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.3	A37/A37A	-3	CTCACC (SEQ ID NO:101)	6	GTGCAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)



Figure 42A

CLONE #	VR	#DEL	VR END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGAGA (SEQ ID NO:112)	18	TGTATCGTACTTACT (SEQ ID NO:113)	D3-10	19	TGTATCGTACTTACT (SEQ ID NO:113)	2	GT (SEQ ID NO:114)	JH4B	-4	CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGAGA (SEQ ID NO:112)	18	TGTATCGTACTTACT (SEQ ID NO:113)	D3-10	19	TGTATCGTACTTACT (SEQ ID NO:113)	2	GT (SEQ ID NO:114)	JH4B	-4	CTTTGA (SEQ ID NO:115)



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				#n				
1.6.1	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.2	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)

Figure 42B





Figure 43A

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.17.1	DP-603-33	0	GAGAGA (SEQ ID NO:1121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:1122)	9	ATATGCTG G (SEQ ID NO:1123)	JH8	-1	TTACTACT (SEQ ID NO:1124)
1.17.2	DP-603-33	0	GAGAGA (SEQ ID NO:1121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:1122)	9	ATATGCTG G (SEQ ID NO:1123)	JH8	-1	TTACTACT (SEQ ID NO:1124)
1.17.3	DP-603-33	0	GAGAGA (SEQ ID NO:1121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:1122)	9	ATATGCTG G (SEQ ID NO:1123)	JH8	-1	TTACTACT (SEQ ID NO:1124)
1.18	DP-161-8	1	CGAGAG (SEQ ID NO:1125)	1	A	D6-18	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:1126)	4	GACA (SEQ ID NO:1123)	JH8	-2	TACTAC (SEQ ID NO:1127)
1.24.1	DP-603-33	0	GAGAGA (SEQ ID NO:1128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:1129)	2	GT (SEQ ID NO:1130)	JH8	-4	CTACTA (SEQ ID NO:1131)
1.24.2	DP-603-33	0	GAGAGA (SEQ ID NO:1128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:1129)	2	GT (SEQ ID NO:1130)	JH8	-4	CTACTA (SEQ ID NO:1131)
1.25.1	DP-795-61	0	GAGAGA (SEQ ID NO:1131)	6	TGGATC (SEQ ID NO:1132)	D3-10	30	GTATATTA TGGTTCAG AGATTAAT ATAA (SEQ ID NO:1133)	3	TGT (SEQ ID NO:1134)	JH8	-4	CTTTGA (SEQ ID NO:1135)

Figure 43B

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.25.2	DP-73/6-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGATTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	4	CTTTGA (SEQ ID NO:134)
1.29	DP-73/6-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATGT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGACA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	4	CTACTA (SEQ ID NO:142)
1.38.1	DP-60/5-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/6-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaATTGG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	4	CTTTGA (SEQ ID NO:150)
1.39.2	DP-73/6-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaATTGG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	4	CTTTGA (SEQ ID NO:150)



Figure 43C

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.40.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.40.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-16/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.48.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATGGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG	7	TGTTGAA	D21-9	20	TATTACTA	1	T	JH4B	0	ACTACT



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Figure 43D

CLONE #	VH	#DEL	VH END (SEQ ID NO:160)	#N's	N Sequence (SEQ ID NO:161)	DH	Size of D	D Sequence (SEQ ID NO:162)	#N's	N Sequence	JH	#del	JH Segment (SEQ ID NO:163)
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A TGCTCTACG (SEQ ID NO:166)	3	GCT	JH8B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A TGCTCTACG (SEQ ID NO:166)	3	GCT	JH8B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-18	31	TATGATTA CGTTTGGa GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-18	31	TATGATTA CGTTTGGa GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	VK	#del	VK end	#n	N SEQ	JK	#del	JK end
1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)





Figure 43E

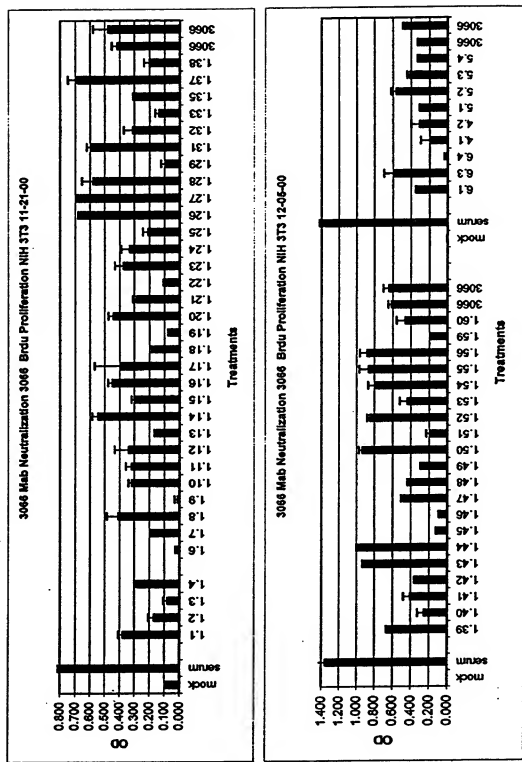
CLONE	Vk	#del	Vk end	#n	N SEQ	JK	#del	JK end
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTGAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.26.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.26.2	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.28	A3/A18/DPK ..	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCAG (SEQ ID NO:181)	JK2	-7	TTTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.38.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)

Figure 43F

CLONE	Vk	#del	Vk end #n	N SEQ	JK	#del	JK end
1.39.2	A30	3	TTACCC (SEQ ID NO:1187)	0	JK1	0	GTGGAC (SEQ ID NO:1188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:1189)	0	JK3	0	ATTGAC (SEQ ID NO:1190)
1.46.1	A30	0	CCCTCC (SEQ ID NO:1191)	0	JK1	-3	GACGTT (SEQ ID NO:1192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:1193)	0	JK1	-3	GACGTT (SEQ ID NO:1193)
1.48.1	L5/DPK5V	1	TCCGTC (SEQ ID NO:1193)	0	JK1	-2	GGACGTT (SEQ ID NO:1194)
1.48.2	L5/DPK5V	1	TCCGTC (SEQ ID NO:1193)	0	JK1	-2	GGACGTT (SEQ ID NO:1194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:1195)	0	JK5	-1	ATGACC (SEQ ID NO:1196)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:1195)	0	JK5	-1	ATGACC (SEQ ID NO:1196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1197)	T	JK3	0	ATTGAC (SEQ ID NO:1198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1197)	T	JK3	0	ATTGAC (SEQ ID NO:1198)



FIGURE 44



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FIGURE 45

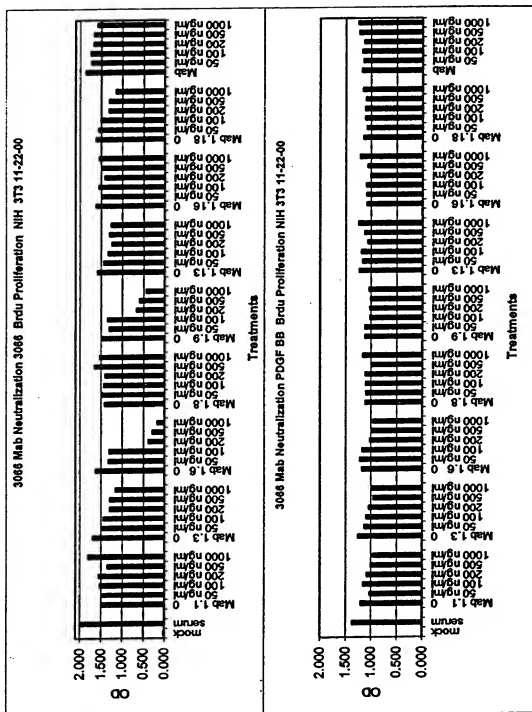


FIGURE 46

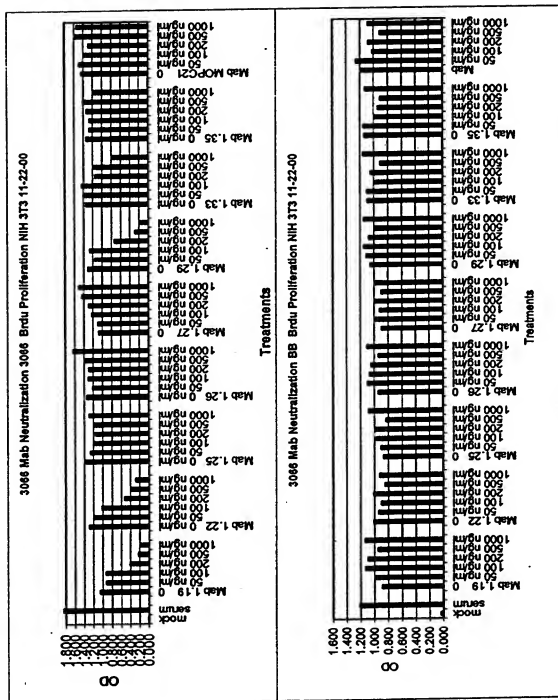
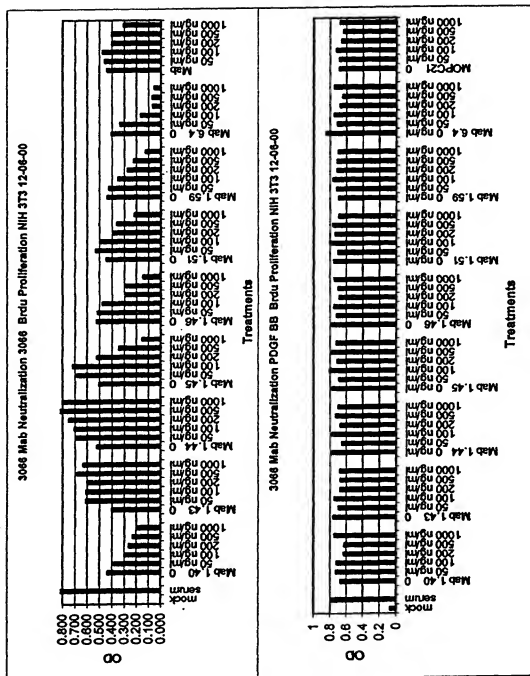


FIGURE 47



ANTIBODIES DIRECTED TO PDGFB AND USES THEREOF
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FIGURE 48

1.19	H	1	Q	A	A	V	V	K	T	D	N	T	Q	WMNPNNSGN	G	60	
6.4	H	1	Q	A	A	V	V	K	T	D	N	T	Q	WMNPNNSGN	D	60	
1.18	H	1	Q	A	A	V	V	K	T	D	N	T	Q	WMNPNNSGN	G	60	
1.40	H	1	Q	A	A	V	V	K	T	T	D	N	T	Q	WMNPNNSGN	G	60
1.45	H	1	Q	A	A	V	V	K	T	D	N	T	Q	WMNPNNSGN	G	60	
1.46	H	1	Q	A	A	V	V	K	S	D	N	T	Q	WMNPNNSGN	G	60	
1.49	H	1	Q	A	A	V	V	K	T	D	N	T	Q	WMNPNNSGD	G	60	
1.33	H	1	Q	A	A	V	V	K	T	G	S	P	Q	WISAYNGN	N	60	
1.48	H	1	Q	A	A	V	V	K	T	G	S	P	Q	WISAYNGN	N	60	
1.6	H	1	E	E	GGLV	G	LRL	A	FN	RT	NMN	P	K	VSSISSSSSNIY		60	
1.17	H	1	Q	E	GG VQ	K	LRL	A	FT	S	GMH	P	K	VAVIWDGNSNKY		60	
1.24	H	1	Q	E	GG VQ	R	LRL	A	FS	S	GMH	P	K	VADIWDGNSNKY		60	
1.38	H	1	Q	E	GG VQ	R	LRL	A	FT	S	GMH	P	K	VAVIWDGNSDKY		60	
1.11	H	1	E	E	GGLIQ	G	LRL	A	FTVS	NYMS		P	K	VSVIYSGGS-	Y	59	
1.23	H	1	E	A	A	E	L	I	EG	S	W	G	MP	K	IIYPGDSR	R	60
1.25	H	1	E	A	A	E	L	I	KG	R	W	G	MP	K	IIYPGDSR	R	60
1.29	H	1	E	A	A	E	L	I	KG	S	W	G	MP	K	IIYPGDSR	R	60
1.39	H	1	E	T	A	E	L	I	KG	R	W	G	MP	K	IIYPGDSR	R	60
1.51	H	1	E	A	A	E	L	I	KG	S	W	G	MP	K	IIYPGDSDAK		60

[CDR1] [CDR2]

1.19	H	61	QKF	V	MTRNT	I	MELS	SE	V	--DVM-ITFGGVIVH-	YGM	V	116
6.4	H	61	QKF	V	MTRDT	I	MELS	SE	I V	--GFG-YSYN-YD	-YGM	V	115
1.18	H	61	QKF	V	MTRNT	I	MELS	SE	V	--EG--IAGVAGTY	YGM	V	116
1.40	H	61	QKF	V	MTRNT	L	MELS	SE	V	--DIV-VVVAATN	-NGM	V	116
1.45	H	61	QKF	V	MTRNT	I	MELS	SE	V	--GSG-YSYG-YD	-YGM	V	115
1.46	H	61	QKF	V	MTRNT	I	MELS	SE	V	--DIV-VVVIATD	-YGM	V	116
1.49	H	61	QKF	V	MTRNT	I	MELS	SE	V F	--MRD-IVATSYL	YGM	V	117
1.33	H	61	QKL	V	MTTDT	T	MELR	SD	V	--DHY-YDSSDYL	YYGL	V	117
1.48	H	61	QKL	V	MTTDT	T	MELR	SD	V	DVEYY-YDGGSYY	FDY	----	115
1.6	H	61	DSVK	F	ISRDN	AKNSL	LQMN	AE	V	DIMI---TFG-GIIASFYF	Y	116	
1.17	H	61	DSVK	F	ISRDN	KN L	LQMN	AE	V	DQGY---RYA-GY	DYGM	V	116
1.24	H	61	DSVK	F	ISRDN	KN L	LQMN	AE	V	DQGY---SYG-YV	DYGM	V	116
1.38	H	61	DSVK	F	VSRDN	KN L	LQMN	AE	V	GYYYD---SSD-YL	YGM	V	117
1.11	H	60	DSVK	F	ISRDN	KN L	LQMN	AE	V	GTVTT-----N	YGM	V	110
1.23	H	61	SPSF	QV	ISADK	I	LQWS	KAS	M	HVSY---YVVS	-NVF	Y	116
1.25	H	61	SPSF	QV	ISADK	I	LQWS	KAS	M	HGSY---YVVS	-NVF	Y	116
1.29	H	61	SPSF	QA	ISADK	I	LQWS	KAS	M	HVDVGATIGGYY	-HGM	V	119
1.39	H	61	SPSF	QV	ISADK	I	LQWS	KAS	M	HGSY---YVVS	-NVF	Y	116
1.51	H	61	SPSF	QV	ISADK	I	LQWS	KAS	M	HYDY---VWRNRY	T-GWF	P	116

CDR3

[CDR3]



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FIGURE 48 (CONT)

1.19	H	117	T	126
6.4	H	116	T	125
1.18	H	117	T	126
1.40	H	117	T	126
1.45	H	116	T	125
1.46	H	117	T	126
1.49	H	118	T	127
1.33	H	118	T	127
1.48	H	116	L	125
1.6	H	117	L	126
1.17	H	117	T	126
1.24	H	117	T	126
1.38	H	118	T	127
1.11	H	111	T	120
1.23	H	117	L	126
1.25	H	117	L	126
1.29	H	120	T	129
1.39	H	117	L	126
1.51	H	117	L	126



FIGURE 49

1.48 L 1		V		T	SS-----W A	A KL	I Q 55
1.49 L 1	V	L	PVTP EPAS	S	S LLHNSNGYNY D LL	QS QL	LG SRA 60
1.11 L 1	V	L	PVTP EPAS	S	S LLQSNNGYNY D L	QS QL	LG NRA 60
1.29 L 1	V	L	PVTP EPAS	S	S LLHNSNGYNY D L	QS QL	LG NRA 60
1.45 L 1				N	SN-----D A	V KL	T Q 55
1.33 L 1				T	SN-----Y A	V KL	T Q 55
1.38 L 1				T	SN-----Y A	V NL	T Q 55
6.4 L 1	E VL	GT	L P E A LS	SVSSS-----Y A	QA RL	T SRA 56	
1.51 L 1	E VL	GT	L P E A LS	SVSSS-----Y A	QA RL	G NRA 56	
1.19 L 1				T	RN-----D G	A KR	S Q 55
1.18 L 1				T	RN-----D G	A KR	S Q 55
1.16 L 1				T	RN-----D G F	A KR	S Q 55
1.23 L 1				T	RN-----D G	I A KR	S Q 55
1.25 L 1				T	RN-----D G	A KR	S Q 55
1.39 L 1				T	RN-----D G	A KR	S Q 55
1.17 L 1				T	RN-----D G	A KR	S Q 55
1.24 L 1				T	RN-----D G	A KR	S Q 55
1.46 L 1				T	RN-----D G	A KR F	S P 55

[CDR1] [CDR2]

1.48 L 56			D	F S	Q SN F R -	Q	107
1.49 L 61		D	D K	RVEA VGV	M TLQITIT--	Q RL	111
1.11 L 61		D	D K	RVEA VGV	M ALQTLT--	G	111
1.29 L 61		D	D K	RVEAD VGV	M ALQSLMCS	Q L	113
1.45 L 56	L		D	V T	QKYN A F -	P D	107
1.33 L 56			D	V T	QKYN A L -	G	107
1.38 L 56			D S	V A	QKCN A W -	Q T	107
6.4 L 57	T I D		R E	F V	Q YG S CS-	Q L	108
1.51 L 57	T I D		R E	F V	Q YG SLF -	P D	108
1.19 L 56			D	F T	L HN D CS-	Q L R	107
1.18 L 56			E	F T F	L HN Y F -	P D	107
1.16 L 56			E	F T	L HN Y L -	G	107
1.23 L 56	R		E	F T	L HN Y W -	Q	107
1.25 L 56			E	F T	L HN Y W -	Q	107
1.39 L 56			E	F T	L HN Y W -	Q	107
1.17 L 56			E	F T	L HN Y L -	G	107
1.24 L 56			E	F T	L HN Y W -	Q	107
1.46 L 56			E	F T	L HSGY P -	Q	107

[CDR3]



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[illegible]

[CDR1]

[CDR2]

1.19 H	61				DVMITGG-VIVH	119	
6.4 H	61		D		IFGYSYN--YD	118	
1.18 H	61			I	V	EGIAVAGT-YY	
1.40 H	61		L			DIVVVVAA-TN	N
1.45 H	61					GSGSYG--YD	118
1.46 H	61					DIVVVVTA-TD	119
1.49 H	61			F		MRDIVATSYYY	F
							120

[CDR3]

1.19 H	120	126
6.4 H	119	125
1.18 H	120	126
1.40 H	120	126
1.45 H	119	125
1.46 H	120	126
1.49 H	121	127



FIGURE 51

1.33 H 1
1.48 H 1

60
60

[CDR1]

[CDR2]

1.33 H 61
1.48 H 61

--DH S D L YY GLDV 118
DVEY G G Y FD ---- 116
[CDR3]

1.33 H 119 T 127
1.48 H 117 L 125



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FIGURE 52

1.17 H 1	K	T	V	SN	60
1.24 H 1	R	S	D	SN	60
1.38 H 1	R	T	I	ND	60
		[CDR1]	[CDR2]		
1.17 H 61	I		DQC -RYAGY D		119
1.24 H 61	I		DQC -SYGYV D		119
1.38 H 61	V		GYG DSSDYL Y		120
			[CDR3]		
1.17 H 120	126				
1.24 H 120	126				
1.38 H 121	127				



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FIGURE 53

1.23 H 1		E	S		60		
1.25 H 1			R		60		
1.29 H 1			S		60		
1.39 H 1			R		60		
1.51 H 1			S		60		
	T				AK 60		
		[CDR1]	[CDR2]
1.23 H 61				VS YVSG---S	NV Y 117		
1.25 H 61				GS YYGSE---T	NV Y 117		
1.29 H 61				VDVGATIGGYYY	HGM V 120		
1.39 H 61				GS YYNSG---S	NV Y 117		
1.51 H 61				YD VWRNY---R	TGW P 117		
				[CDR3]	
1.23 H 118					126		
1.25 H 118					126		
1.29 H 121					129		
1.39 H 118					126		
1.51 H 118					126		
	T						



FIGURE 54

1.49 L 1
1.11 L 1
1.29 L 1

H	L	S	60
Q	Q	N	60
H	Q	N	60
[CDR1]		[CDR2]	

1.49 L 61
1.11 L 61
1.29 L 61

E	T	TIT--	Q	RL	111
E	A	TLT--	G	KV	111
D	A	SLMCS	Q	KL	113
[CDR3]					



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FIGURE 55

1.45 L 1
1.33 L 1
1.38 L 1

N	D	K	L	60
T	Y	K	S	60
T	Y	N	S	60

[CDR1]

[CDR2]

1.45 L 61
1.33 L 61
1.38 L 61

T	T	Y	F	P	K	D	107
T	T	Y	L	G	K	E	107
S	A	C	W	Q	T	E	107

[CDR3]



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FIGURE 56

6.4 L 1
1.51 L 1

[CDR1]

AT S 60
GA N 60
[CDR2]

6.4 L 61
1.51 L 61

PCS Q LE 108
LFT P VD 108
[CDR3]

1.19	L	1
1.18	L	1
1.16	L	1
1.23	L	1
1.25	L	1
1.39	L	1
1.17	L	1
1.24	L	1
1.46	L	1

F				60
	I		R	60
				60
				60
				60
		F	P	60

[CDR1] [CDR2]

```
1.19 L 61
1.18 L 61
1.16 L 61
1.23 L 61
1.25 L 61
1.39 L 61
1.17 L 61
1.24 L 61
1.46 L 61
```

D

	D	CS	Q	L	R	107
F		F	P	D		107
		L	G			107
		W	Q			107
		W	Q			107
		W	Q			107
		L	G			107
		W	Q			107
	SG	P	Q			107
	[CDR3]			